



2394 Pr seq list.ST25.txt  
SEQUENCE LISTING

<110> Alcon, Inc.  
Yanni, John M.  
Gamache, Daniel A.  
Miller, Steven T.

<120> Treatment of Dry Eye in Postmenopausal Women by Restoring 15-lipoxygenase Activity to Ocular Surface Cells

<130> 2394

<160> 10

<170> PatentIn version 3.1

(1) GENERAL INFORMATION:  
(iii) NUMBER OF SEQUENCES: 10

<210> INFORMATION FOR SEQ ID NO:1:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2671 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

aagatgggtc tctaccgcat ccgcgtgtcc actggggcct cgctctatgc cggttccaac	60
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aacgtccggg ccaggactgg gctgggtctct gacatgggaa ttttcgacca gataatgagc	1260

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actggtgggg gaggccacgt gcagctgctc aagcaagctg gagccttcct aacctacaga 1320
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<210> INFORMATION FOR SEQ ID NO:2:

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 661 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Gly Leu Tyr Arg Ile Arg Val Ser Thr Gly Ala Ser Leu Tyr Ala
1           5           10           15

Gly Ser Asn Asn Gln Val Gln Leu Trp Leu Val Gly Gln His Gly Glu
20           25           30

Ala Ala Leu Gly Lys Arg Leu Trp Pro Ala Arg Gly Glu Thr Glu Leu
35           40           45

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Lys Val Glu Val Pro Glu Tyr Leu Gly Pro Leu Leu Phe Val Lys Leu  
50 55 60

Arg Lys Arg His Leu Leu Lys Asp Asp Ala Trp Phe Cys Asn Trp Ile  
65 70 75 80

Ser Val Gln Gly Pro Gly Ala Gly Asp Glu Val Arg Phe Pro Cys Tyr  
85 90 95

Arg Trp Val Glu Gly Asn Gly Val Leu Ser Leu Pro Glu Gly Thr Gly  
100 105 110

Arg Thr Val Gly Glu Asp Pro Gln Gly Leu Phe Gln Lys His Arg Glu  
115 120 125

Glu Glu Leu Glu Glu Arg Arg Lys Leu Tyr Arg Trp Gly Asn Trp Lys  
130 135 140

Asp Gly Leu Ile Leu Asn Met Ala Gly Ala Lys Leu Tyr Asp Leu Pro  
145 150 155 160

Val Asp Glu Arg Phe Leu Glu Asp Lys Arg Val Asp Phe Glu Val Ser  
165 170 175

Leu Ala Lys Gly Leu Ala Asp Leu Ala Ile Lys Asp Ser Leu Asn Val  
180 185 190

Leu Thr Cys Trp Lys Asp Leu Asp Asp Phe Asn Arg Ile Phe Trp Cys  
195 200 205

Gly Gln Ser Lys Leu Ala Glu Arg Val Arg Asp Ser Trp Lys Glu Asp  
210 215 220

Ala Leu Phe Gly Tyr Gln Phe Leu Asn Gly Ala Asn Pro Val Val Leu  
225 230 235 240

Arg Arg Ser Ala His Leu Pro Ala Arg Leu Val Phe Pro Pro Gly Met  
245 250 255

Glu Glu Leu Gln Ala Gln Leu Glu Lys Glu Leu Glu Gly Gly Thr Leu  
260 265 270

Phe Glu Ala Asp Phe Ser Leu Leu Asp Gly Ile Lys Ala Asn Val Ile  
275 280 285

Leu Cys Ser Gln Gln His Leu Ala Ala Pro Leu Val Met Leu Lys Leu  
290 295 300

Gln Pro Asp Gly Lys Leu Leu Pro Met Val Ile Gln Leu Gln Leu Pro  
305 310 315 320

Arg Thr Gly Ser Pro Pro Pro Pro Leu Phe Leu Pro Thr Asp Pro Pro

Met Ala Trp Leu Leu Ala Lys Cys Trp Val Arg Ser Ser Asp Phe Gln  
340 345 350

Leu His Glu Leu Gln Ser His Leu Leu Arg Gly His Leu Met Ala Glu  
355 360 365

Val Ile Val Val Ala Thr Met Arg Cys Leu Pro Ser Ile His Pro Ile  
370 375 380

Phe Lys Leu Ile Ile Pro His Leu Arg Tyr Thr Leu Glu Ile Asn Val  
385 390 395 400

Arg Ala Arg Thr Gly Leu Val Ser Asp Met Gly Ile Phe Asp Gln Ile  
405 410 415

Met Ser Thr Gly Gly Gly Gly His Val Gln Leu Leu Lys Gln Ala Gly  
420 425 430

Ala Phe Leu Thr Tyr Ser Ser Phe Cys Pro Pro Asp Asp Leu Ala Asp  
435 440 445

Arg Gly Leu Leu Gly Val Lys Ser Ser Phe Tyr Ala Gln Asp Ala Leu  
450 455 460

Arg Leu Trp Glu Ile Ile Tyr Arg Tyr Val Glu Gly Ile Val Ser Leu  
465 470 475 480

His Tyr Lys Thr Asp Val Ala Val Lys Asp Asp Pro Glu Leu Gln Thr  
485 490 495

Trp Cys Arg Glu Ile Thr Glu Ile Gly Leu Gln Gly Ala Gln Asp Arg  
500 505 510

Gly Phe Pro Val Ser Leu Gln Ala Arg Asp Gln Val Cys His Phe Val  
515 520 525

Thr Met Cys Ile Phe Thr Cys Thr Gly Gln His Ala Ser Val His Leu  
530 535 540

Gly Gln Leu Asp Trp Tyr Ser Trp Val Pro Asn Ala Pro Cys Thr Met  
545 550 555 560

Arg Leu Pro Pro Pro Thr Thr Lys Asp Ala Thr Leu Glu Thr Val Met  
565 570 575

Ala Thr Leu Pro Asn Phe His Gln Ala Ser Leu Gln Met Ser Ile Thr  
580 585 590

Trp Gln Leu Gly Arg Arg Gln Pro Val Met Val Ala Val Gly Gln His  
595 600 605

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Glu Glu Glu Tyr Phe Ser Gly Pro Glu Pro Lys Ala Val Leu Lys Lys  
610 615 620

Phe Arg Glu Glu Leu Ala Ala Leu Asp Lys Glu Ile Glu Ile Arg Asn  
625 630 635 640

Ala Lys Leu Asp Met Pro Tyr Glu Tyr Leu Arg Pro Ser Val Val Glu  
645 650 655

Asn Ser Val Ala Ile  
660

<210> INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3224 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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tgaagaagac ttcgaggtga cgcttcccc ggacgtaggc actgtgctga tgctgcgagt	240
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caagggcacg agggagagga accgaggcct ggcactgccc tacacctacc tggatcctcc	2040
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tggagaaca tatctgctct tccagatgac cagggtagct cacagccatg tgtcattcta	2640
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aaccatctgt aatgggatcc gatgccctct tctggcgtgt ctgaagacag cgacagtgt	2880
tgcacatata taaaataaat aaatcttta aaaacaaaac aagagagagg gacatgctac	2940
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ttgcagagag ttagaagata ttctcaaacc tctaatacct tcacatctaa aatccatctt	3060
cattccaaaa ttccaatatt ttatatacac tctccagttt ggtgggtgag gggttgtttt	3120
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<210> INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 677 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Lys Cys Arg Val Arg Val Ser Thr Gly Glu Ala Cys Gly Ala  
 1 5 10 15  
 Gly Thr Trp Asp Lys Val Ser Val Ser Ile Val Gly Thr His Gly Glu  
 20 25 30  
 Ser Pro Leu Val Pro Leu Asp His Leu Gly Lys Glu Phe Ser Ala Gly  
 35 40 45  
 Ala Glu Glu Asp Phe Glu Val Thr Leu Pro Gln Asp Val Gly Thr Val  
 50 55 60  
 Leu Met Leu Arg Val His Lys Ala Pro Pro Glu Val Ser Leu Pro Leu  
 65 70 75 80  
 Met Ser Phe Arg Ser Asp Ala Trp Phe Cys Arg Trp Phe Glu Leu Glu  
 85 90 95  
 Trp Leu Pro Gly Ala Ala Leu His Phe Pro Cys Tyr Gln Trp Leu Glu  
 100 105 110  
 Gly Ala Gly Glu Leu Val Leu Arg Glu Gly Ala Ala Lys Val Ser Trp  
 115 120 125  
 Gln Asp His His Pro Thr Leu Gln Asp Gln Arg Gln Lys Glu Leu Glu  
 130 135 140  
 Ser Arg Gln Lys Met Tyr Ser Trp Lys Thr Tyr Ile Glu Gly Trp Pro  
 145 150 155 160  
 Arg Cys Leu Asp His Glu Thr Val Lys Asp Leu Asp Leu Asn Ile Lys  
 165 170 175  
 Tyr Ser Ala Met Lys Asn Ala Lys Leu Phe Phe Lys Ala His Ser Ala  
 180 185 190  
 Tyr Thr Glu Leu Lys Val Lys Gly Leu Leu Asp Arg Thr Gly Leu Trp  
 195 200 205  
 Arg Ser Leu Arg Glu Met Arg Arg Leu Phe Asn Phe Arg Lys Thr Pro  
 210 215 220  
 Ala Ala Glu Tyr Val Phe Ala His Trp Gln Glu Asp Ala Phe Phe Ala  
 225 230 235 240  
 Ser Gln Phe Leu Asn Gly Ile Asn Pro Val Leu Ile Arg Arg Cys His  
 245 250 255  
 Ser Leu Pro Asn Asn Phe Pro Val Thr Asp Glu Met Val Ala Pro Val  
 260 265 270

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Leu Gly Pro Gly Thr Ser Leu Gln Ala Glu Leu Glu Lys Gly Ser Leu  
275 280 285

Phe Leu Val Asp His Gly Ile Leu Ser Gly Val His Thr Asn Ile Leu  
290 295 300

Asn Gly Lys Pro Gln Phe Ser Ala Ala Pro Met Thr Leu Leu His Gln  
305 310 315 320

Ser Ser Gly Ser Gly Pro Leu Leu Pro Ile Ala Ile Gln Leu Lys Gln  
325 330 335

Thr Pro Gly Pro Asp Asn Pro Ile Phe Leu Pro Ser Asp Asp Thr Trp  
340 345 350

Asp Trp Leu Leu Ala Lys Thr Trp Val Arg Asn Ser Glu Phe Tyr Ile  
355 360 365

His Glu Ala Val Thr His Leu Leu His Ala His Leu Ile Pro Glu Val  
370 375 380

Phe Ala Leu Ala Thr Leu Arg Gln Leu Pro Arg Cys His Pro Leu Phe  
385 390 395 400

Lys Leu Leu Ile Pro His Ile Arg Tyr Thr Leu His Ile Asn Thr Leu  
405 410 415

Ala Arg Glu Leu Leu Val Ala Pro Gly Lys Leu Ile Asp Lys Ser Thr  
420 425 430

Gly Leu Gly Thr Gly Gly Phe Ser Asp Leu Ile Lys Arg Asn Met Glu  
435 440 445

Gln Leu Asn Tyr Ser Val Leu Cys Leu Pro Glu Asp Ile Arg Ala Arg  
450 455 460

Gly Val Glu Asp Ile Pro Gly Tyr Tyr Tyr Arg Asp Asp Gly Met Gln  
465 470 475 480

Ile Trp Gly Ala Ile Lys Ser Phe Val Ser Glu Ile Val Ser Ile Tyr  
485 490 495

Tyr Pro Ser Asp Thr Ser Val Gln Asp Asp Gln Glu Leu Gln Ala Trp  
500 505 510

Val Arg Glu Ile Phe Ser Glu Gly Phe Leu Gly Arg Glu Ser Ser Gly  
515 520 525

Met Pro Ser Leu Leu Asp Thr Arg Glu Ala Leu Val Gln Tyr Ile Thr  
530 535 540



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Met Val Ile Phe Thr Cys Ser Ala Lys His Ala Ala Val Ser Ser Gly  
545 550 555 560

Gln Phe Asp Ser Cys Val Trp Met Pro Asn Leu Pro Pro Thr Met Gln  
565 570 575

Leu Pro Pro Pro Thr Ser Lys Gly Gln Ala Arg Pro Glu Ser Phe Ile  
580 585 590

Ala Thr Leu Pro Ala Val Asn Ser Ser Ser Tyr His Ile Ile Ala Leu  
595 600 605

Trp Leu Leu Ser Ala Glu Pro Gly Asp Gln Arg Pro Leu Gly His Tyr  
610 615 620

Pro Asp Glu His Phe Thr Glu Asp Ala Pro Arg Arg Ser Val Ala Ala  
625 630 635 640

Phe Gln Arg Lys Leu Ile Gln Ile Ser Lys Gly Ile Arg Glu Arg Asn  
645 650 655

Arg Gly Leu Ala Leu Pro Tyr Thr Tyr Leu Asp Pro Pro Leu Ile Glu  
660 665 670

Asn Ser Val Ser Ile  
675

<210> INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

gcgctgcggc tctgggaaat catct

25

<210> INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala Leu Arg Leu Trp Glu Ile Ile  
1 5

<210> INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

gggcccgaaa aatactcctc ctcac

25

<210> INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Glu Glu Glu Tyr Phe Ser Gly Pro  
1 5

<210> INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ctacccaagt gatgagtctg tc

22

<210> INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

tgttccccctg ggatttagat gga

23